

SEQUENCE LISTING

<110> Arnaut, Greta
Boets, Annemie
Vanneste, Stijn
Van Rie, Jeroen
Van Houdt, Sara

<120> Novel Bacillus thuringiensis insecticidal proteins

<130> 58764.000036

<150> US 09/756,296

<151> 2001-01-09

<160> 9

<170> PatentIn version 3.0

<210> 1

<211> 1899

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(1896)

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Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp	
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acc atc cga aaa gaa tgg atg gag tgg aaa aga aca gat cat agt tta	144
Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu	
35 40 45	

tat gta gct cct ata gtc gga act gtt tct agc ttt ctg cta aag aag	192
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gtg ggg agt ctt att gga aaa agg ata ttg agt gaa tta tgg ggg tta	240
Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu	
65 70 75 80	

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Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu	
85 90 95	

aca gaa caa ttc cta aat caa aga ctt aat aca gac act ctt gcc cgt	336
Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg	
100 105 110	

gta aat gcg gaa ttg gaa ggg ctg caa gcg aat ata agg gag ttt aat	384
Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn	
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Ile	Glu	Ser	Pro	Ser	Gly	Thr	Pro	Gly	Gly	Leu	Arg	Ala	Tyr	Met	Val	
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Asn	Gly	Arg	Val	Tyr	Thr	Ala	Ser	Asn	Val	Asn	Thr	Thr	Thr	Asn	Asn	
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1899

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 35 40 45

Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys Lys
 50 55 60

Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly Leu
 65 70 75 80

Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
 85 90 95

Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
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Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe Asn
 115 120 125

Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro Leu
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Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
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Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
 165 170 175

Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val Val
 180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
 195 200 205

Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys Ile
 210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
 225 230 235 240

Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
 245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
 260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
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Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser
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Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe
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Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu
 325 330 335

Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly
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Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu
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Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly
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Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser Thr
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Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr
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Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
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Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg Asn
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Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
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Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
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Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
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Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
515 520 525

Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu
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Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn
565 570 575

Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn Met Gly
580 585 590

Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val
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Pro Thr Asn Leu Pro Pro Ile Tyr
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<222> (1) .. (1896)

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Asn Val Val Ala His Asp Pro Phe Ser Phe Gln His Lys Ser Leu Asp	
20 25 30	
acc ata caa gaa gaa tgg atg gag tgg aaa aaa gat aat cat agt tta	144
Thr Ile Gln Glu Glu Trp Met Glu Trp Lys Lys Asp Asn His Ser Leu	
35 40 45	
tat gta gat cct att gtt gga act gtg gct agt ttt ctt tta aag aaa	192
Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys	
50 55 60	
gtg ggg agt ctt gtt gga aaa aga ata ctg agt gag tta cgg aat tta	240
Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu	
65 70 75 80	
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Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu	
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Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg	
100 105 110	
gta aat gcg gaa ttg aca ggg ctg caa gca aat gta gaa gag ttt aat	384
Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn	
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Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu	
130 135 140	
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Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile	
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ctt aat gca gac gaa tgg gga att tca gca gca aca tta cgt acg tat	624
Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr	
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caa aat cac ctg aga aat tat aca aga gat tac tct aat tat tgt ata	672
Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile	
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Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser	
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gaa aaa ttt gga aat caa ggt gat tcc tta aga ttt gaa caa agc aac	1584
Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn	
515 520 525	
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Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu	
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Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr Ile	
545 550 555 560	
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Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn	
565 570 575	
gat gga gtt aat gat aat gga gct cgt ttt tca gat att aat att ggt	1776
Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly	
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595 600 605	
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35 40 45	
Tyr Val Asp Pro Ile Val Gly Thr Val Ala Ser Phe Leu Leu Lys Lys	

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60

Val Gly Ser Leu Val Gly Lys Arg Ile Leu Ser Glu Leu Arg Asn Leu
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Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg Glu
85 90 95

Thr Glu Lys Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala Arg
100 105 110

Val Asn Ala Glu Leu Thr Gly Leu Gln Ala Asn Val Glu Glu Phe Asn
115 120 125

Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Arg Asn Ala Val Pro Leu
130 135 140

Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn Arg
145 150 155 160

Leu Thr Gln Phe Gln Met Gln Gly Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr Tyr
195 200 205

Gln Asn His Leu Arg Asn Tyr Thr Arg Asp Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His Asp
225 230 235 240

Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser Phe
275 280 285

Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn Ser

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295

300

Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr Phe
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Pro Asn Ile Val Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu Leu
325 330 335

Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile Gly
340 345 350

Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro Leu
355 360 365

Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg Gly
370 375 380

Gly Ile Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Thr Thr
385 390 395 400

Leu Gly Leu Arg Ser Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn Tyr
405 410 415

Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val Val
420 425 430

Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Gln Ile Arg Asn
435 440 445

Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met Val
450 455 460

Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn Gly
465 470 475 480

Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile Ser
485 490 495

Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser
500 505 510

Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln Ser Asn
515 520 525

Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr Asn Leu
530 535 540

Tyr Leu Arg Val Ser Ser Ile Gly Asn Ser Thr Ile Arg Val Thr Ile
545 550 555 560

Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr Asn Asn
565 570 575

Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly
580 585 590

Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile Asn Val
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Pro Thr Asn Ile Ser Pro Leu Tyr
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Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp
20 25 30

acc ata caa aaa gaa tgg atg gag tgg aaa aga act gat cat agt tta 144
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu
35 40 45

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Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys
50 55 60

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Ile Phe Pro Ser Gly Ser Ile Glu Ser Met Gln Asp Ile Leu Arg Gly
85 90 95

gca gaa caa ttt cta aat caa aga ctt gat gca gac acc ttt agt cgt	336
Ala Glu Gln Phe Leu Asn Gln Arg Leu Asp Ala Asp Thr Phe Ser Arg	
100 105 110	
gta gaa gca gaa ttg aga ggg ctt caa gca aat gta gag gaa ttt aat	384
Val Glu Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe Asn	
115 120 125	
cga caa gtg gac aat ttt tta aac cca aat caa aac cct gcc cct tta	432
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu	
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Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr	
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Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val	
245 250 255	
tct atc tgg tcg ttg ttt aaa tat cag agc ctt ctg gta tcc tct ggc	816
Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly	
260 265 270	
gct aat tta tat gcg agt ggt agt gga gta aca aat aga caa tca ttt	864
Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe	
275 280 285	
act gca caa gac tgg cca ttt tta aat tct ctt ttc caa gtt aat caa	912
Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln	
290 295 300	
aat tat gta tta aca ggt atg aat ggt tat agg tat act tta agt tct	960
Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser	
305 310 315 320	
gtt ttt ggt aca aat caa aca ata cat tct gtt agg agt aat tat agg	1008
Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg	
325 330 335	
ggc ggg gtt tca tct ggt tac att gga gtt aat ctt agt gaa ggt gac	1056

Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp	
340 345 350	
caa aat ttt agt tgt agt aca ttt ttg gat cct tta gaa aca ccg ttt	1104
Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe	
355 360 365	
att aga agt tgg ctg gat tca ggt agc gat gat ggc ttt aat tgg agt	1152
Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser	
370 375 380	
aca gga gtc ttt aca aca act att ggt tta cct act tgt agc att ttt	1200
Thr Gly Val Phe Thr Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe	
385 390 395 400	
tgg cct cgt ggt aac tcg aac tat ttt cca gat tat ttt ata cga aat	1248
Trp Pro Arg Gly Asn Ser Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn	
405 410 415	
att tct ggt gtc gtt ggt cgt ctt agg aac gaa gat tta aga aga cca	1296
Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro	
420 425 430	
cta tat ttt aat gag ata aga aat ata gta gga aat aac aat cca ccg	1344
Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Asn Pro Pro	
435 440 445	
gca act gga tcg tta tca gtc gcc agc cta gtc tct gtg cat aac aga	1392
Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg	
450 455 460	
aaa aat aat att tat gct gct cat gaa aat ggt act atg att cat ttg	1440
Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu	
465 470 475 480	
gca ccg gaa gat tat aca ggt ttc aca atg tca cca ata cat gca act	1488
Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr	
485 490 495	
caa gta aat aat caa aca cga aca ttt att tcc gag aaa tta gga aac	1536
Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn	
500 505 510	
caa ggt gat tcc ttg aga ttt gaa caa aca aat aca acg gct cga tac	1584
Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Thr Ala Arg Tyr	
515 520 525	
aca ttt aga ggg aat gga aat agt tac aat ctt tat tta aga gta tct	1632
Thr Phe Arg Gly Asn Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser	
530 535 540	
tca cta gga aat tcc aca att cga gtt act ata aac ggt aga gtt tat	1680
Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr	
545 550 555 560	
act gtt tca aac gtc aat act act aca aat aac gat gga gtt gtt gat	1728
Thr Val Ser Asn Val Asn Thr Thr Thr Asn Asn Asp Gly Val Val Asp	
565 570 575	
aat ggc gct cgt ttt tca gat att aat ata ggt aat gta gtg gca agt	1776
Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser	

580	585	590	
gct aat act aat ata cca tta gat ata aat gta aca ttt aac tct ggt			1824
Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly			
595	600	605	
acg caa ttt gag ctt atg aat att atg ttt gtt cca act aat att cca			1872
Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro			
610	615	620	
cca att tat taa			1884
Pro Ile Tyr			
625			

<210> 6
 <211> 627
 <212> PRT
 <213> Bacillus thuringiensis
 <400> 6

Met Asn Asn Val Leu Asn Ser Glu Arg Thr Thr Lys Cys Gly Ala Tyr	
1 5 10 15	
Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu Asp	
20 25 30	
Thr Ile Gln Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser Leu	
35 40 45	
Tyr Val Ser Pro Ile Val Gly Thr Ile Ala Ser Phe Leu Leu Lys Lys	
50 55 60	
Ile Gly Gly Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Lys Asn Leu	
65 70 75 80	
Ile Phe Pro Ser Gly Ser Ile Glu Ser Met Gln Asp Ile Leu Arg Gly	
85 90 95	
Ala Glu Gln Phe Leu Asn Gln Arg Leu Asp Ala Asp Thr Phe Ser Arg	
100 105 110	
Val Glu Ala Glu Leu Arg Gly Leu Gln Ala Asn Val Glu Glu Phe Asn	
115 120 125	
Arg Gln Val Asp Asn Phe Leu Asn Pro Asn Gln Asn Pro Ala Pro Leu	
130 135 140	
Ala Ile Ile Asp Ser Val Asn Thr Leu Gln Gln Leu Phe Leu Ser Arg	
145 150 155 160	

Leu Pro Gln Phe Gln Ile Gln Arg Tyr Gln Leu Leu Leu Leu Pro Leu
165 170 175

Phe Ala Gln Ala Ala Asn Leu His Leu Ser Phe Ile Arg Asp Val Ile
180 185 190

Leu Asn Ala Asp Glu Trp Gly Ile Pro Ala Ala Thr Val Arg Thr Tyr
195 200 205

Arg Glu His Leu Gln Arg Tyr Thr Arg Glu Tyr Ser Asn Tyr Cys Ile
210 215 220

Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Ala Thr Leu His Asp
225 230 235 240

Phe Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Leu Asp Tyr Val
245 250 255

Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser Gly
260 265 270

Ala Asn Leu Tyr Ala Ser Gly Ser Gly Val Thr Asn Arg Gln Ser Phe
275 280 285

Thr Ala Gln Asp Trp Pro Phe Leu Asn Ser Leu Phe Gln Val Asn Gln
290 295 300

Asn Tyr Val Leu Thr Gly Met Asn Gly Tyr Arg Tyr Thr Leu Ser Ser
305 310 315 320

Val Phe Gly Thr Asn Gln Thr Ile His Ser Val Arg Ser Asn Tyr Arg
325 330 335

Gly Gly Val Ser Ser Gly Tyr Ile Gly Val Asn Leu Ser Glu Gly Asp
340 345 350

Gln Asn Phe Ser Cys Ser Thr Phe Leu Asp Pro Leu Glu Thr Pro Phe
355 360 365

Ile Arg Ser Trp Leu Asp Ser Gly Ser Asp Asp Gly Phe Asn Trp Ser
370 375 380

Thr Gly Val Phe Thr Thr Thr Ile Gly Leu Pro Thr Cys Ser Ile Phe
385 390 395 400

Trp Pro Arg Gly Asn Ser Asn Tyr Phe Pro Asp Tyr Phe Ile Arg Asn
 405 410 415

Ile Ser Gly Val Val Gly Arg Leu Arg Asn Glu Asp Leu Arg Arg Pro
 420 425 430

Leu Tyr Phe Asn Glu Ile Arg Asn Ile Val Gly Asn Asn Asn Pro Pro
 435 440 445

Ala Thr Gly Ser Leu Ser Val Ala Ser Leu Val Ser Val His Asn Arg
 450 455 460

Lys Asn Asn Ile Tyr Ala Ala His Glu Asn Gly Thr Met Ile His Leu
 465 470 475 480

Ala Pro Glu Asp Tyr Thr Gly Phe Thr Met Ser Pro Ile His Ala Thr
 485 490 495

Gln Val Asn Asn Gln Thr Arg Thr Phe Ile Ser Glu Lys Leu Gly Asn
 500 505 510

Gln Gly Asp Ser Leu Arg Phe Glu Gln Thr Asn Thr Thr Ala Arg Tyr
 515 520 525

Thr Phe Arg Gly Asn Gly Asn Ser Tyr Asn Leu Tyr Leu Arg Val Ser
 530 535 540

Ser Leu Gly Asn Ser Thr Ile Arg Val Thr Ile Asn Gly Arg Val Tyr
 545 550 555 560

Thr Val Ser Asn Val Asn Thr Thr Thr Asn Asn Asp Gly Val Val Asp
 565 570 575

Asn Gly Ala Arg Phe Ser Asp Ile Asn Ile Gly Asn Val Val Ala Ser
 580 585 590

Ala Asn Thr Asn Ile Pro Leu Asp Ile Asn Val Thr Phe Asn Ser Gly
 595 600 605

Thr Gln Phe Glu Leu Met Asn Ile Met Phe Val Pro Thr Asn Ile Pro
 610 615 620

Pro Ile Tyr
 625

<210> 7

<211> 1910
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> artificial cry2Ae DNA sequence for expression in cotton

 <220>
 <221> CDS
 <222> (3)..(1901)

 <400> 7

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Met Ala Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp	
1 5 10 15	
 gca tac aac gtt gtt gct cat gat cct ttc tct ttc gag cat aag tct	95
Ala Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser	
20 25 30	
 ctt gat aca att agg aag gag tgg atg gag tgg aag agg act gat cat	143
Leu Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His	
35 40 45	
 tct ctt tac gtt gct cct att gtt ggt act gtt tct tct ttc ctt ctt	191
Ser Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu	
50 55 60	
 aag aag gtt ggt tct ctt atc ggt aag agg atc ctt tct gag ctt tgg	239
Lys Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp	
65 70 75	
 ggt ctt atc ttc cct tct ggt tct act aac ctt atg caa gat att ctt	287
Gly Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu	
80 85 90 95	
 agg gag act gaa caa ttc ctt aac cag agg ctt aac act gat act ctt	335
Arg Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu	
100 105 110	
 gct agg gtt aac gct gag ctt gag ggt ctt caa gct aac att agg gaa	383
Ala Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu	
115 120 125	
 ttc aac cag caa gtt gat aac ttc ctt aac cct act caa aac cct gtt	431
Phe Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val	
130 135 140	
 cct ctt tct att act tct tct gtt aac act atg caa caa ctt ttc ctt	479
Pro Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu	
145 150 155	
 aac agg ctt cct caa ttc agg gtt caa ggt tac caa ctt ctt ctt ctt	527
Asn Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu	
160 165 170 175	
 cct ctt ttc gct caa gct gct aac atg cac cta agc ttc att agg gat	575
Pro Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp	
180 185 190	

Val Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile
435 440 445

agg aac att gag tct cct tct ggt act cct ggt ggt ctt agg gct tac 1391
Arg Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr
450 455 460

atg gtt tct gtt cat aac agg aag aac aac atc tac gct gtt cat gag 1439
Met Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu
465 470 475

aac ggt act atg att cat ctt gct cct gag gat tac acc ggt ttc acc 1487
Asn Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr
480 485 490 495

atc tcc ccc atc cac gcc acc cag gtc aat aat cag acc agg acc ttc 1535
Ile Ser Pro Ile His Ala Thr Gln Val Asn Asn Gln Thr Arg Thr Phe
500 505 510

atc tcc gag aag ttc ggc aac cag ggc gac tcc ctg agg ttc gag cag 1583
Ile Ser Glu Lys Phe Gly Asn Gln Gly Asp Ser Leu Arg Phe Glu Gln
515 520 525

tcc aac acc acc gcc agg tac acc ctg agg ggc aac ggc aac tcc tac 1631
Ser Asn Thr Thr Ala Arg Tyr Thr Leu Arg Gly Asn Gly Asn Ser Tyr
530 535 540

aac ctg tac ctc agg gtg tcc tcc ctc ggc aac tcc acc atc agg gtc 1679
Asn Leu Tyr Leu Arg Val Ser Ser Leu Gly Asn Ser Thr Ile Arg Val
545 550 555

acc atc aac ggc agg gtg tac acc gcc tcc aac gtg aac acc acc acc 1727
Thr Ile Asn Gly Arg Val Tyr Thr Ala Ser Asn Val Asn Thr Thr Thr
560 565 570 575

aac aac gac ggc gtc aac gac aac ggc gct agg ttc ctg gac atc aac 1775
Asn Asn Asp Gly Val Asn Asp Asn Gly Ala Arg Phe Leu Asp Ile Asn
580 585 590

atg ggc aac gtc gtg gcc tcc gac aac acc aac gtg ccc ctg gac atc 1823
Met Gly Asn Val Val Ala Ser Asp Asn Thr Asn Val Pro Leu Asp Ile
595 600 605

aac gtg aca ttt aac tcc ggc acc cag ttc gag ctg atg aac atc atg 1871
Asn Val Thr Phe Asn Ser Gly Thr Gln Phe Glu Leu Met Asn Ile Met
610 615 620

ttc gtg cca act aac ctc cca ccc atc tac tgagctagc 1910
Phe Val Pro Thr Asn Leu Pro Pro Ile Tyr
625 630

<210> 8
<211> 633
<212> PRT
<213> Artificial Sequence

<400> 8

Met Ala Asn Asn Val Leu Asn Asn Gly Arg Thr Thr Ile Cys Asp Ala
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Tyr Asn Val Val Ala His Asp Pro Phe Ser Phe Glu His Lys Ser Leu
20 25 30

Asp Thr Ile Arg Lys Glu Trp Met Glu Trp Lys Arg Thr Asp His Ser
35 40 45

Leu Tyr Val Ala Pro Ile Val Gly Thr Val Ser Ser Phe Leu Leu Lys
50 55 60

Lys Val Gly Ser Leu Ile Gly Lys Arg Ile Leu Ser Glu Leu Trp Gly
65 70 75 80

Leu Ile Phe Pro Ser Gly Ser Thr Asn Leu Met Gln Asp Ile Leu Arg
85 90 95

Glu Thr Glu Gln Phe Leu Asn Gln Arg Leu Asn Thr Asp Thr Leu Ala
100 105 110

Arg Val Asn Ala Glu Leu Glu Gly Leu Gln Ala Asn Ile Arg Glu Phe
115 120 125

Asn Gln Gln Val Asp Asn Phe Leu Asn Pro Thr Gln Asn Pro Val Pro
130 135 140

Leu Ser Ile Thr Ser Ser Val Asn Thr Met Gln Gln Leu Phe Leu Asn
145 150 155 160

Arg Leu Pro Gln Phe Arg Val Gln Gly Tyr Gln Leu Leu Leu Leu Pro
165 170 175

Leu Phe Ala Gln Ala Ala Asn Met His Leu Ser Phe Ile Arg Asp Val
180 185 190

Val Leu Asn Ala Asp Glu Trp Gly Ile Ser Ala Ala Thr Leu Arg Thr
195 200 205

Tyr Gln Asn Tyr Leu Lys Asn Tyr Thr Thr Glu Tyr Ser Asn Tyr Cys
210 215 220

Ile Asn Thr Tyr Gln Thr Ala Phe Arg Gly Leu Asn Thr Arg Leu His
225 230 235 240

Asp Met Leu Glu Phe Arg Thr Tyr Met Phe Leu Asn Val Phe Glu Tyr
245 250 255

Val Ser Ile Trp Ser Leu Phe Lys Tyr Gln Ser Leu Leu Val Ser Ser
260 265 270

Gly Ala Asn Leu Tyr Ala Ser Gly Ser Gly Pro Gln Gln Thr Gln Ser
275 280 285

Phe Thr Ser Gln Asp Trp Pro Phe Leu Tyr Ser Leu Phe Gln Val Asn
290 295 300

Ser Asn Tyr Val Leu Asn Gly Phe Ser Gly Ala Arg Leu Thr Gln Thr
305 310 315 320

Phe Pro Asn Ile Gly Gly Leu Pro Gly Thr Thr Thr Thr His Ala Leu
325 330 335

Leu Ala Ala Arg Val Asn Tyr Ser Gly Gly Val Ser Ser Gly Asp Ile
340 345 350

Gly Ala Val Phe Asn Gln Asn Phe Ser Cys Ser Thr Phe Leu Pro Pro
355 360 365

Leu Leu Thr Pro Phe Val Arg Ser Trp Leu Asp Ser Gly Ser Asp Arg
370 375 380

Gly Gly Val Asn Thr Val Thr Asn Trp Gln Thr Glu Ser Phe Glu Ser
385 390 395 400

Thr Leu Gly Leu Arg Cys Gly Ala Phe Thr Ala Arg Gly Asn Ser Asn
405 410 415

Tyr Phe Pro Asp Tyr Phe Ile Arg Asn Ile Ser Gly Val Pro Leu Val
420 425 430

Val Arg Asn Glu Asp Leu Arg Arg Pro Leu His Tyr Asn Glu Ile Arg
435 440 445

Asn Ile Glu Ser Pro Ser Gly Thr Pro Gly Gly Leu Arg Ala Tyr Met
450 455 460

Val Ser Val His Asn Arg Lys Asn Asn Ile Tyr Ala Val His Glu Asn
465 470 475 480

Gly Thr Met Ile His Leu Ala Pro Glu Asp Tyr Thr Gly Phe Thr Ile
485 490 495